

## SEQUENCE LISTING

<110> Hinuma, Shuji  
MARUYAMA, Minoru  
FUJII, Ryo

<120> Novel Use of EDG Receptor

<130> 3127USOP

<150> PCT/JP2003/015836

<151> 2003-12-11

<150> JP 2002-361415

<151> 2002-12-12

<160> 45

<210> 1

<211> 364

<212> PRT

<213> human

<400> 1

Met	Ala	Ala	Ile	Ser	Thr	Ser	Ile	Pro	Val	Ile	Ser	Gln	Pro	Gln	Phe
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Thr	Ala	Met	Asn	Glu	Pro	Gln	Cys	Phe	Tyr	Asn	Glu	Ser	Ile	Ala	Phe
			20					25					30		
Phe	Tyr	Asn	Arg	Ser	Gly	Lys	His	Leu	Ala	Thr	Glu	Trp	Asn	Thr	Val
			35					40					45		
Ser	Lys	Leu	Val	Met	Gly	Leu	Gly	Ile	Thr	Val	Cys	Ile	Phe	Ile	Met
			50					55					60		
Leu	Ala	Asn	Leu	Leu	Val	Met	Val	Ala	Ile	Tyr	Val	Asn	Arg	Arg	Phe
			65					70					75		80
His	Phe	Pro	Ile	Tyr	Tyr	Leu	Met	Ala	Asn	Leu	Ala	Ala	Ala	Asp	Phe
								85					90		95
Phe	Ala	Gly	Leu	Ala	Tyr	Phe	Tyr	Leu	Met	Phe	Asn	Thr	Gly	Pro	Asn

100	105	110
Thr Arg Arg Leu Thr Val Ser Thr Trp Leu Leu Arg Gln Gly Leu Ile		
115	120	125
Asp Thr Ser Leu Thr Ala Ser Val Ala Asn Leu Leu Ala Ile Ala Ile		
130	135	140
Glu Arg His Ile Thr Val Phe Arg Met Gln Leu His Thr Arg Met Ser		
145	150	155
Asn Arg Arg Val Val Val Val Ile Val Val Ile Trp Thr Met Ala Ile		
165	170	175
Val Met Gly Ala Ile Pro Ser Val Gly Trp Asn Cys Ile Cys Asp Ile		
180	185	190
Glu Asn Cys Ser Asn Met Ala Pro Leu Tyr Ser Asp Ser Tyr Leu Val		
195	200	205
Phe Trp Ala Ile Phe Asn Leu Val Thr Phe Val Val Met Val Val Leu		
210	215	220
Tyr Ala His Ile Phe Gly Tyr Val Arg Gln Arg Thr Met Arg Met Ser		
225	230	235
Arg His Ser Ser Gly Pro Arg Arg Asn Arg Asp Thr Met Met Ser Leu		
245	250	255
Leu Lys Thr Val Val Ile Val Leu Gly Ala Phe Ile Ile Cys Trp Thr		
260	265	270
Pro Gly Leu Val Leu Leu Leu Leu Asp Val Cys Cys Pro Gln Cys Asp		
275	280	285
Val Leu Ala Tyr Glu Lys Phe Phe Leu Leu Leu Ala Glu Phe Asn Ser		
290	295	300
Ala Met Asn Pro Ile Ile Tyr Ser Tyr Arg Asp Lys Glu Met Ser Ala		
305	310	315
Thr Phe Arg Gln Ile Leu Cys Cys Gln Arg Ser Glu Asn Pro Thr Gly		
325	330	335
Pro Thr Glu Gly Ser Asp Arg Ser Ala Ser Ser Leu Asn His Thr Ile		
340	345	350
Leu Ala Gly Val His Ser Asn Asp His Ser Val Val		
355	360	

&lt;210&gt; 2

&lt;211&gt; 1092

&lt;212&gt; DNA

&lt;213&gt; human

&lt;400&gt; 2

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atggctgcca tctctacttc catccctgta atttcacagc cccagttcac agccatgaat   60
gaaccacagt gcttctacaa cgagtcatt gccttctttt ataaccgaag tggaaagcat   120
cttgccacag aatggaacac agtcagcaag ctggatgatg gacttggaat cactgtttgt   180
atcttcatca tgttgccaa cctattggtc atggtgga tctatgtcaa ccgccgttc   240
cattttccta tttattacct aatggcta atggctgtg cagacttctt tgctgggttg   300
gcctacttct atctcatgtt caacacagga cccaatactc ggagactgac tgtagcaca   360
tggtccctgc gtcaggcct cattgacacc agcctgacgg catctgtggc caacttacig   420
gctattgcaa tcgagaggca cattacggtt ttccgatgc agtccacac acggatgagc   480
aaccggcggg tagtggtggt cattgtggtc atctggacta tggccatcgt tatgggtgct   540
ataccagtg tgggctggaa ctgtatctgt gatattgaaa attgttcaa catggcaccc   600
ctctacagtg actcttactt agtcttctgg gccattttca acttggtgac ctttgtggta   660
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cggcatagtt ctggaccccg gcggaatcgg gataccatga tgagtcttct gaagactgtg   780
gtcattgtgc ttggggcctt tatcatctgc tggactcctg gatiggtttt gttacttcta   840
gacgtgtgct gtccacagtg cgacgtgtg gcctatgaga aattcttctt tctccttgct   900
gaattcaact ctgcatgaa cccatcatt tactcctacc gcgacaaaga aatgagcgcc   960
acctttaggc agatcctctg ctgccagcgc agtgagaacc ccaccggccc cacagaaggc  1020
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cactctgtgg tt                                     1092

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&lt;210&gt; 3

&lt;211&gt; 364

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 3

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Met Ala Ala Ala Ser Thr Ser Ser Pro Val Ile Ser Gln Pro Gln Phe
      5              10              15
Thr Ala Met Asn Glu Gln Gln Cys Phe Tyr Asn Glu Ser Ile Ala Phe
      20              25              30
Phe Tyr Asn Arg Ser Gly Lys Tyr Leu Ala Thr Glu Trp Asn Thr Val
      35              40              45
Ser Lys Leu Val Met Gly Leu Gly Ile Thr Val Cys Val Phe Ile Met
      50              55              60

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Leu Ala Asn Leu Leu Val Met Val Ala Ile Tyr Val Asn Arg Arg Phe  
 65 70 75 80  
 His Phe Pro Ile Tyr Tyr Leu Met Ala Asn Leu Ala Ala Asp Phe  
 85 90 95  
 Phe Ala Gly Leu Ala Tyr Phe Tyr Leu Met Phe Asn Thr Gly Pro Asn  
 100 105 110  
 Thr Arg Arg Leu Thr Val Ser Thr Trp Leu Leu Arg Gln Gly Leu Ile  
 115 120 125  
 Asp Thr Ser Leu Thr Ala Ser Val Ala Asn Leu Leu Ala Ile Ala Ile  
 130 135 140  
 Glu Arg His Ile Thr Val Phe Arg Met Gln Leu His Thr Arg Met Ser  
 145 150 155 160  
 Asn Arg Arg Val Val Val Val Ile Val Val Ile Trp Thr Met Ala Ile  
 165 170 175  
 Val Met Gly Ala Ile Pro Ser Val Gly Trp Asn Cys Ile Cys Asp Ile  
 180 185 190  
 Asp His Cys Ser Asn Met Ala Pro Leu Tyr Ser Asp Ser Tyr Leu Val  
 195 200 205  
 Phe Trp Ala Ile Phe Asn Leu Val Thr Phe Val Val Met Val Val Leu  
 210 215 220  
 Tyr Ala His Ile Phe Gly Tyr Val Arg Gln Arg Thr Met Arg Met Ser  
 225 230 235 240  
 Arg His Ser Ser Gly Pro Arg Arg Asn Arg Asp Thr Met Met Ser Leu  
 245 250 255  
 Leu Lys Thr Val Val Ile Val Leu Gly Ala Phe Ile Val Cys Trp Thr  
 260 265 270  
 Pro Gly Leu Val Leu Leu Leu Leu Asp Val Cys Cys Pro Gln Cys Asp  
 275 280 285  
 Val Leu Ala Tyr Glu Lys Phe Phe Leu Leu Leu Ala Glu Phe Asn Ser  
 290 295 300  
 Ala Met Asn Pro Ile Ile Tyr Ser Tyr Arg Asp Lys Glu Met Ser Ala  
 305 310 315 320  
 Thr Phe Arg Gln Ile Leu Cys Cys Gln Arg Asn Glu Asn Pro Asn Gly  
 325 330 335  
 Pro Thr Glu Gly Ser Asp Arg Ser Ala Ser Ser Leu Asn His Thr Ile  
 340 345 350  
 Leu Ala Gly Val His Ser Asn Asp His Ser Val Val

355

360

&lt;210&gt; 4

&lt;211&gt; 1092

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 4

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atggcagctg cctctacttc cagccctgtg atttcacagc cccagttcac agccatgaac   60
gaacaacagt gcttctacaa cgagtctatc gccttcttct ataaccggag tggaaagtat   120
ctagccacag aatggaacac tgtgagcaag ctggtgatgg gactgggcat cactgtctgc   180
gtgttcatca tcttgcccaa tctactggtc atggtggcaa tttacgtcaa ccgccgttc   240
catttcccta tttattactt gatggccaac ctggtgtctg cagacttctt cgctggactg   300
gcctacttct accgatgtt caacacggga cctaataccc ggagactgac cgtgagcaca   360
tggtctctcc ggcagggcct catcgacacc agcctgaagg cttctgtggc caacctgtg   420
gccattgcca tcgagaggca catcacagt ttcggaatgc agctccatac acgaatgagc   480
aaccgacgtg tgggtggtgt gattgtagtc atctggacta tggccattgt gatgggtgcc   540
ataccacgtg tgggctggaa ctgcatctgt gatatcgatc attgttccaa catggcgccc   600
ctctacagtg actcctactt agtcttctgg gccattttca acctgggtgac ctttgtggtc   660
atggtgggtc tctacgtca catctttggc tatgttcgcc agaggactat gagaatgtcc   720
cggcatagtt ctggaccag gaggaatcgg gacaccatga tgagccttct gaagactgtg   780
gtcattgtgc tgggtgcctt tattgtctgc tggactccgg gatttgtctt gctactgtc   840
gatgtgtgtt gcccgagtg cgatgtcctg gcctatgaga agttcttctt cctcctggcc   900
gagttcaact ctgctatgaa ccccatcacc tactcctacc gcgacaaaga gatgagcgcc   960
accttcaggc agatcctgtg ttgccagcgc aacgagaacc ccaacggccc cacggaaggc  1020
tctgaccgct cggcctctc cctcaaccac actattctgg ctggagttca cagcaatgac  1080
cactctgtgg tt                                     1092

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&lt;210&gt; 5

&lt;211&gt; 378

&lt;212&gt; PRT

&lt;213&gt; human

&lt;400&gt; 5

Met Ala Thr Ala Leu Pro Pro Arg Leu Gln Pro Val Arg Gly Asn Glu

5

10

15

Thr Leu Arg Glu His Tyr Gln Tyr Val Gly Lys Leu Ala Gly Arg Leu

20	25	30
Lys Glu Ala Ser Glu Gly Ser Thr Leu Thr Thr Val Leu Phe Leu Val		
35	40	45
Ile Cys Ser Phe Ile Val Leu Glu Asn Leu Met Val Leu Ile Ala Ile		
50	55	60
Trp Lys Asn Asn Lys Phe His Asn Arg Met Tyr Phe Phe Ile Gly Asn		
65	70	75
80		
Leu Ala Leu Cys Asp Leu Leu Ala Gly Ile Ala Tyr Lys Val Asn Ile		
85	90	95
Leu Met Ser Gly Lys Lys Thr Phe Ser Leu Ser Pro Thr Val Trp Phe		
100	105	110
Leu Arg Glu Gly Ser Met Phe Val Ala Leu Gly Ala Ser Thr Cys Ser		
115	120	125
Leu Leu Ala Ile Ala Ile Glu Arg His Leu Thr Met Ile Lys Met Arg		
130	135	140
Pro Tyr Asp Ala Asn Lys Arg His Arg Val Phe Leu Leu Ile Gly Met		
145	150	155
160		
Cys Trp Leu Ile Ala Phe Thr Leu Gly Ala Leu Pro Ile Leu Gly Trp		
165	170	175
Asn Cys Leu His Asn Leu Pro Asp Cys Ser Thr Ile Leu Pro Leu Tyr		
180	185	190
Ser Lys Lys Tyr Ile Ala Phe Cys Ile Ser Ile Phe Thr Ala Ile Leu		
195	200	205
Val Thr Ile Val Ile Leu Tyr Ala Arg Ile Tyr Phe Leu Val Lys Ser		
210	215	220
Ser Ser Arg Lys Val Ala Asn His Asn Asn Ser Glu Arg Ser Met Ala		
225	230	235
240		
Leu Leu Arg Thr Val Val Ile Val Val Ser Val Phe Ile Ala Cys Trp		
245	250	255
Ser Pro Leu Phe Ile Leu Phe Leu Ile Asp Val Ala Cys Arg Val Gln		
260	265	270
Ala Cys Pro Ile Leu Phe Lys Ala Gln Trp Phe Ile Val Leu Ala Val		
275	280	285
Leu Asn Ser Ala Met Asn Pro Val Ile Tyr Thr Leu Ala Ser Lys Glu		
290	295	300
Met Arg Arg Ala Phe Phe Arg Leu Val Cys Asn Cys Leu Val Arg Gly		
305	310	315
320		

Arg Gly Ala Arg Ala Ser Pro Ile Gln Pro Ala Leu Asp Pro Ser Arg  
 325 330 335  
 Ser Lys Ser Ser Ser Ser Asn Asn Ser Ser His Ser Pro Lys Val Lys  
 340 345 350  
 Glu Asp Leu Pro His Thr Asp Pro Ser Ser Cys Ile Met Asp Lys Asn  
 355 360 365  
 Ala Ala Leu Gln Asn Gly Ile Phe Cys Asn  
 370 375

<210> 6

<211> 1134

<212> DNA

<213> human

<400> 6

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ctcaccaccg tgcctcttctt ggtcatctgc agcttcatcg tcttggagaa cctgatggtt 180
ttgattgcc a tctggaaaaa caataaat t cacaaccgca tgtacttttt cattggcaac 240
ctggctctct ggcacctgct ggccggcatc gcttacaagg tcaacattct gatgtctggc 300
aagaagacgt tcagcctgtc tcccacggtc tggttcctca gggaggggcag tatgttcgtg 360
gcccttgggg cgtccacctg cagcttactg gccatcgcca tcgagcggca cttgacaatg 420
atcaaaatga ggccttacga cgccaacaag aggcaccgag tcttctctct gatcgggatg 480
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aatctccctg actgctctac cactctgccc ctctactcca agaagtacat tgccttctgc 600
atcagcatct tcaaggccat cctggtgacc atcgtgatec tctacgcacg catctacttc 660
ctgggtgaagt ccagcagccg taaggtggcc aaccacaaca actcggagcg gtccatggca 720
ctgctgcgga ccgtggtgat tgtggtgagc gtgttcatcg cctgctggtc cccactcttc 780
atcctcttcc tcattgatgt ggcttcagg gtgcaggcgt gcccacacct cttcaaggct 840
cagtgttca tcgtgttggc tgtgtcaac tccgcatga acccggtcat ctacacgctg 900
gccagcaagg agatgcggcg ggccttcttc cgtctggtct gcaactgcct ggtcagggga 960
cggggggccc ggcctcacc catccagcct gcgtctgacc caagcagaag taaatcaagc 1020
agcagcaaca atagcagcca ctctccgaag gtcaaggaag acctgcccc caacagacccc 1080
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<210> 7

<211> 222

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 7

Arg Met Tyr Phe Phe Ile Gly Asn Leu Ala Leu Cys Asp Leu Leu Ala  
                     5                    10                    15  
 Gly Ile Ala Tyr Lys Val Asn Ile Leu Met Ser Gly Arg Lys Thr Phe  
                     20                    25                    30  
 Ser Leu Ser Pro Thr Val Trp Phe Leu Arg Glu Gly Ser Met Phe Val  
                     35                    40                    45  
 Ala Leu Gly Ala Ser Thr Cys Ser Leu Leu Ala Ile Ala Ile Glu Arg  
                     50                    55                    60  
 His Leu Thr Met Ile Lys Met Arg Pro Tyr Asp Ala Asn Lys Lys His  
                     65                    70                    75                    80  
 Arg Val Phe Leu Leu Ile Gly Met Cys Trp Leu Ile Ala Phe Ser Leu  
                     85                    90                    95  
 Gly Ala Leu Pro Ile Leu Gly Trp Asn Cys Leu Glu Asn Phe Pro Asp  
                     100                    105                    110  
 Cys Ser Thr Ile Leu Pro Leu Tyr Ser Lys Lys Tyr Ile Ala Phe Leu  
                     115                    120                    125  
 Ile Ser Ile Phe Thr Ala Ile Leu Val Thr Ile Val Ile Leu Tyr Ala  
                     130                    135                    140  
 Arg Ile Tyr Phe Leu Val Lys Ser Ser Ser Arg Arg Val Ala Asn His  
                     145                    150                    155                    160  
 Asn Ser Glu Arg Ser Met Ala Leu Leu Arg Thr Val Val Ile Val Val  
                     165                    170                    175  
 Ser Val Phe Ile Ala Cys Trp Ser Pro Leu Phe Ile Leu Phe Leu Ile  
                     180                    185                    190  
 Asp Val Ala Cys Arg Ala Lys Glu Cys Ser Ile Leu Phe Lys Ser Gln  
                     195                    200                    205  
 Trp Phe Ile Met Leu Ala Val Leu Asn Ser Ala Met Asn Pro  
                     210                    215                    220

&lt;210&gt; 8

&lt;211&gt; 666

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 8

```

cgcatgtact ttttcattgg caacttggt ctctgcgacc tgcggccgg catagcctac   60
aaggtcaaca ttctgatgtc cggtaggaag acgttcagcc tgtctccaac agtgtggttc  120
ctcagggagg gcagtatgtt cgtagccctg ggcgcacca catgcagctt attggccatt  180
gccattgagc ggcacctgac catgatcaag atgaggccgt acgacgcaa caagaagcac  240
cgcggtttcc ttctgattgg gatgtgctgg ctaattgcct tctcgctggg tgccctgcc  300
atcctgggct ggaactgcct ggagaacttt cccgactgct ctaccatctt gcccctctac  360
tccaagaaat acattgcctt tctcatcagc atcttcacag ccattctggt gaccatcgtc  420
atcttgtacg cgcgcacctt cttcctggtc aagtccagca gccgcagggt ggccaaccac  480
aactccgaga gatccatggc ctttctcggg accgtagtga tcgtggtgag cgtgttcac  540
gcctgttggt cccccctttt catcctcttc ctcacgatg tggcctgcag ggccaaggag  600
tgcctcatcc tcttcaagag tcagtgggtc atcatgtgg ctgtctcaa ctccgccatg  660
aaccaca

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&lt;210&gt; 9

&lt;211&gt; 353

&lt;212&gt; PRT

&lt;213&gt; human

&lt;400&gt; 9

```

Met Gly Ser Leu Tyr Ser Glu Tyr Leu Asn Pro Asn Lys Val Gln Glu
      5              10              15
His Tyr Asn Tyr Thr Lys Glu Thr Leu Glu Thr Gln Glu Thr Thr Ser
      20              25              30
Arg Gln Val Ala Ser Ala Phe Ile Val Ile Leu Cys Cys Ala Ile Val
      35              40              45
Val Glu Asn Leu Leu Val Leu Ile Ala Val Ala Arg Asn Ser Lys Phe
      50              55              60
His Ser Ala Met Tyr Leu Phe Leu Gly Asn Leu Ala Ala Ser Asp Leu
      65              70              75              80
Leu Ala Gly Val Ala Phe Val Ala Asn Thr Leu Leu Ser Gly Ser Val
      85              90              95
Thr Leu Arg Leu Thr Pro Val Gln Trp Phe Ala Arg Glu Gly Ser Ala
      100             105             110
Ser Ile Thr Leu Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile
      115             120             125

```

Glu Arg His Val Ala Ile Ala Lys Val Lys Leu Tyr Gly Ser Asp Lys  
 130 135 140  
 Ser Cys Arg Met Leu Leu Leu Ile Gly Ala Ser Trp Leu Ile Ser Leu  
 145 150 155 160  
 Val Leu Gly Gly Leu Pro Ile Leu Gly Trp Asn Cys Leu Gly His Leu  
 165 170 175  
 Glu Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys His Tyr Val Leu  
 180 185 190  
 Cys Val Val Thr Ile Phe Ser Ile Ile Leu Leu Ala Ile Val Ala Leu  
 195 200 205  
 Tyr Val Arg Ile Tyr Cys Val Val Arg Ser Ser His Ala Asp Met Ala  
 210 215 220  
 Ala Pro Gln Thr Leu Ala Leu Leu Lys Thr Val Thr Ile Val Leu Gly  
 225 230 235 240  
 Val Phe Ile Val Cys Trp Leu Pro Ala Phe Ser Ile Leu Leu Leu Asp  
 245 250 255  
 Tyr Ala Cys Pro Val His Ser Cys Pro Ile Leu Tyr Lys Ala His Tyr  
 260 265 270  
 Phe Phe Ala Val Ser Thr Leu Asn Ser Leu Leu Asn Pro Val Ile Tyr  
 275 280 285  
 Thr Trp Arg Ser Arg Asp Leu Arg Arg Glu Val Leu Arg Pro Leu Gln  
 290 295 300  
 Cys Trp Arg Pro Gly Val Gly Val Gln Gly Arg Arg Arg Val Gly Thr  
 305 310 315 320  
 Pro Gly His His Leu Leu Pro Leu Arg Ser Ser Ser Ser Leu Glu Arg  
 325 330 335  
 Gly Met His Met Pro Thr Ser Pro Thr Phe Leu Glu Gly Asn Thr Val  
 340 345 350  
 Val

&lt;210&gt; 10

&lt;211&gt; 1059

&lt;212&gt; DNA

&lt;213&gt; human

&lt;400&gt; 10

atgggcagct tgtactcgga gtacctgaac cccaacaagg tccaggaaca ctataattat 60

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accaaggaga cgctggaaac gcaggagacg acctcccgcc aggtggcctc ggccttcac 120
gtcatcctct gttgcgcat tgtggtggaa aaccttctgg tgcctattgc ggtggccga 180
aacagcaagt tccactcggc aatgtacctg tttctgggca acctggccgc ctccgatcta 240
ctggcaggcg tggccttcgt agccaatacc ttgctctctg gctctgtcac gctgaggetg 300
acgcctgtgc agtggtttgc cggggagggc tctgcctcca tcacgtcttc ggcctctgtc 360
ttcagcctcc tggccatcgc cattgagcgc cacgtggcca ttgccaaggt caagctgtat 420
ggcagcgaca agagctgccg catgtttctg ctcatcgagg cctcgtggct catctcgtg 480
gtcctcggtg gcctgcccac ccttggctgg aactgcctgg gccacctcga ggcctgtcc 540
actgtcctgc ctctctacgc caagcattat gtgtgtgctg tggtagcat ctctccac 600
atcctgttgg ccatcgtggc cctgtacgtg cgcctctact gcgtggtcg ctcaagccac 660
gctgacatgg ccgccccgca gacgctagcc ctgtcaaga cggtcaccat cgtgctagc 720
gtctttatcg tctgtggct gccgccttc agcatcctcc ttctggacta tgcctgtccc 780
gtccactcct gcccgatcct ctacaaagcc cactactttt tcgcgtctc caccctgaat 840
tcctgtctca accccgtcat ctacacgtg cgcagccggg acctgcggcg ggaggtgctt 900
cggccgctgc agtgtgtggc gccgggggtg ggggtgcaag gacggaggcg ggtcgggacc 960
ccgggccacc acctcctgcc actccgcagc tccagctccc tggagagggg catgcacatg 1020
cccacgtcac ccacgtttct ggagggaac acggtggtc 1059

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<210> 11

<211> 352

<212> PRT

<213> Rat

<400> 11

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Met Gly Gly Leu Tyr Ser Glu Tyr Leu Asn Pro Glu Lys Val Gln Glu
      5              10              15
His Tyr Asn Tyr Thr Lys Glu Thr Leu Asp Met Gln Glu Thr Pro Ser
      20              25              30
Arg Lys Val Ala Ser Ala Phe Ile Ile Ile Leu Cys Cys Ala Ile Val
      35              40              45
Val Glu Asn Leu Leu Val Leu Ile Ala Val Ala Arg Asn Ser Lys Phe
      50              55              60
His Ser Ala Met Tyr Leu Phe Leu Gly Asn Leu Ala Ala Ser Asp Leu
      65              70              75              80
Leu Ala Gly Val Ala Phe Val Ala Asn Thr Leu Leu Ser Gly Pro Val
      85              90              95
Thr Leu Ser Leu Thr Pro Leu Gln Trp Phe Ala Arg Glu Gly Ser Ala

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100	105	110
Phe Ile Thr Leu Ser Ala Ser Val	Phe Ser Leu Leu Ala Ile Ala Ile	
115	120	125
Glu Arg Gln Val Ala Ile Ala Lys Val	Lys Leu Tyr Gly Ser Asp Lys	
130	135	140
Ser Cys Arg Met Leu Met Leu Ile Gly	Ala Ser Trp Leu Ile Ser Leu	
145	150	155
Ile Leu Gly Gly Leu Pro Ile Leu Gly	Trp Asn Cys Leu Asp His Leu	
165	170	175
Glu Ala Cys Ser Thr Val Leu Pro Leu	Tyr Ala Lys His Tyr Val Leu	
180	185	190
Cys Val Val Thr Ile Phe Ser Val Ile	Leu Leu Ala Ile Val Ala Leu	
195	200	205
Tyr Val Arg Ile Tyr Phe Val Val Arg	Ser Ser His Ala Asp Val Ala	
210	215	220
Gly Pro Gln Thr Leu Ala Leu Leu Lys	Thr Val Thr Ile Val Leu Gly	
225	230	235
Val Phe Ile Ile Cys Trp Leu Pro Ala	Phe Ser Ile Leu Leu Leu Asp	
245	250	255
Ser Thr Cys Pro Val Arg Ala Cys Pro	Val Leu Tyr Lys Ala His Tyr	
260	265	270
Phe Phe Ala Phe Ala Thr Leu Asn Ser	Leu Leu Asn Pro Val Ile Tyr	
275	280	285
Thr Trp Arg Ser Arg Asp Leu Arg Arg	Glu Val Leu Arg Pro Leu Leu	
290	295	300
Cys Trp Arg Gln Gly Lys Gly Ala Thr	Gly Arg Arg Gly Gly Asn Pro	
305	310	315
Gly His Arg Leu Leu Pro Leu Arg Ser	Ser Ser Ser Leu Glu Arg Gly	
325	330	335
Leu His Met Pro Thr Ser Pro Thr Phe	Leu Glu Gly Asn Thr Val Val	
340	345	350

&lt;210&gt; 12

&lt;211&gt; 1056

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 12

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atgggcggtt tatactcaga gtacctcaat cctgagaagg ttcaggaaca ctacaattac   60
accaaggaga cgctggacat gcaggagacg cctccccgca aggtggcctc cgccttcac   120
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